## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

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- (i) APPLICANT: GUERIN-MARCHAND, Claudine DRUILHE, Pierre
- (ii) TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE OF STIMULATING THE T LYMPHOCYTES
- (iii) NUMBER OF SEQUENCES: 46
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Burns, Doane, Swecker & Mathis
  - (B) STREET: P.O. Box 1404
  - (C) CITY: Alexandria
  - (D) STATE: Virginia
  - (E) COUNTRY: United States
  - (F) ZIP: 22313-1404
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/098,327
  - (B) FILING DATE: 24-NOV-1993
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: FR 91 01286
  - (B) FILING DATE: 05-FEB-1991
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: McGowan, Malcolm K.
  - (B) REGISTRATION NUMBER: 39,300
  - (C) REFERENCE/DOCKET NUMBER: 010830-045
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (703) 836-6620
    - (B) TELEFAX: (703) 836-2021
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 8
  - (D) OTHER INFORMATION: /note= "Amino Acid 8 wherein Xaa is Glu or Gly."
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Leu Ala Lys Glu Lys Leu Gln Xaa Gln Gln Ser Asp Leu Glu Gln Glu 1 5 15

Arg

- (2) INFORMATION FOR SEQ ID NO:2:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1
    - (D) OTHER INFORMATION: /note= "Amino Acid 1 wherein Xaa is Ser or Arg."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 6
    - (D) OTHER INFORMATION: /note= "Amino Acid 6 wherein Xaa is Glu or Asp."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 8
    - (D) OTHER INFORMATION: /note= "Amino Acid 8 wherein Xaa is Arg or Leu."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 15
    - (D) OTHER INFORMATION: /note= "Amino Acid 15 wherein Xaa is Glu or Gly."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln 1 5 15

Gln

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- (2) INFORMATION FOR SEQ ID NO:3:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 2
    - (D) OTHER INFORMATION: /note= "Amino Acid 2 wherein Xaa is Ser or Arg."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 7
    - (D) OTHER INFORMATION: /note= "Amino Acid 7 wherein Xaa is Glu or Asp."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 9
    - (D) OTHER INFORMATION: /note= "Amino Acid 9 wherein Xaa is Arg or Leu."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 16
    - (D) OTHER INFORMATION: /note= "Amino Acid 16 wherein Xaa is Glu or Gly."
    - (x) PUBLICATION INFORMATION:
      - (H) DOCUMENT NUMBER: WO 92/13884
      - (J) PUBLICATION DATE: 20-AUG-1992
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa 1 10 15

Gln

- (2) INFORMATION FOR SEQ ID NO:4:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 3
  - (D) OTHER INFORMATION: /note= "Amino Acid 3 wherein Xaa is Ser or Arg."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 8
  - (D) OTHER INFORMATION: /note= "Amino Acid 8 wherein Xaa is Glu or Asp."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 10
  - (D) OTHER INFORMATION: /note= "Amino Acid 10 wherein Xaa is Arg or Leu."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 17
  - (D) OTHER INFORMATION: /note= "Amino Acid 17 wherein Xaa is Glu or Gly."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln 1 5 10 15

Xaa

- (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1
    - (D) OTHER INFORMATION: /note= "Amino Acid 1 wherein Xaa is Glu or Gly."
  - (ix) FEATURE:

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- (A) NAME/KEY: Peptide
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Amino Acid 4 wherein Xaa is Ser or Arg."

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Amino Acid 9 wherein Xaa is Glu or Asp."

### (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Amino Acid 11 wherein Xaa is Arg or Leu."

### (x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: WO 92/13884
- (J) PUBLICATION DATE: 20-AUG-1992

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu

Gln

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# ( <del>2=</del>) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 2
  - (D) OTHER INFORMATION: /note= "Amino Acid 2 wherein Xaa is Glu or Gly."

### (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Amino Acid 5 wherein Xaa is Ser or Arg."

### (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "Amino Acid 10 wherein Xaa is Glu or Asp."

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 12
  - (D) OTHER INFORMATION: /note= "Amino Acid 12 wherein Xaa is Arg or Leu."
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys 1 10 15

Leu

# (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 3
  - (D) OTHER INFORMATION: /note= "Amino Acid 3 wherein Xaa is Glu or Gly."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 6
  - (D) OTHER INFORMATION: /note= "Amino Acid 6 wherein Xaa is Ser or Arg."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 11
  - (D) OTHER INFORMATION: /note= "Amino Acid 11 wherein Xaa is Glu or Asp."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 13
  - (D) OTHER INFORMATION: /note= "Amino Acid 13 wherein Xaa is Arg or Leu."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

 Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu 1 5 15

Lys

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- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 4
    - (D) OTHER INFORMATION: /note= "Amino Acid 4 wherein Xaa is Glu or Gly."
  - (ix) FEATURE:

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- (A) NAME/KEY: Peptide
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "Amino Acid 7 wherein Xaa is Ser or Arg."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 12
  - (D) OTHER INFORMATION: /note= "Amino Acid 12 wherein Xaa is Glu or Asp."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 14
  - (D) OTHER INFORMATION: /note= "Amino Acid 14 wherein Xaa is Arg or Leu."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala Lys 1 5 10 15

Glu

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 5
  - (D) OTHER INFORMATION: /note= "Amino Acid 5 wherein Xaa is Glu or Gly."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 8
  - (D) OTHER INFORMATION: /note= "Amino Acid 8 wherein Xaa is Ser or Arq."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide(B) LOCATION: 13

  - (D) OTHER INFORMATION: /note= "Amino Acid 13 wherein Xaa is Glu or Asp."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 15
  - (D) OTHER INFORMATION: /note= "Amino Acid 15 wherein Xaa is Arg or Leu."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa Ala 10

Lys

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 6
    - (D) OTHER INFORMATION: /note= "Amino Acid 6 wherein Xaa is Glu or Gly."
  - (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Amino Acid 9 wherein Xaa is Ser or Arg."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 14
  - (D) OTHER INFORMATION: /note= "Amino Acid 14 wherein Xaa is Glu or Asp."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 16
  - (D) OTHER INFORMATION: /note= "Amino Acid 16 wherein Xaa is Arg or Leu."
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg Xaa 10

Ala

- ( <del>2=)</del> INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids

    - (B) TYPE: amino acid (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 7
    - (D) OTHER INFORMATION: /note= "Amino Acid 7 wherein Xaa is Glu or Gly."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 10
    - (D) OTHER INFORMATION: /note= "Amino Acid 10 wherein Xaa is Ser or Arg."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 15
    - (D) OTHER INFORMATION: /note= "Amino Acid 15 wherein Xaa is Glu or Asp."

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 17
  - (D) OTHER INFORMATION: /note= "Amino Acid 17 wherein Xaa is Arg or Leu."
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa Arg 1 5 10 15

Xaa

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /note= "Amino Acid 1 wherein Xaa is Arg or Leu."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 8
  - (D) OTHER INFORMATION: /note= "Amino Acid 8 wherein Xaa is Glu or Gly."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 11
  - (D) OTHER INFORMATION: /note= "Amino Acid 11 wherein Xaa is Ser or Arg."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 16
  - (D) OTHER INFORMATION: /note= "Amino Acid 16 wherein Xaa is Glu or Asp."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln Xaa 1 5 10 15

Arg

- (2) INFORMATION FOR SEQ ID NO:13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 2
    - (D) OTHER INFORMATION: /note= "Amino Acid 2 wherein Xaa is Arg or Leu."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 9
    - (D) OTHER INFORMATION: /note= "Amino Acid 9 wherein Xaa is Glu or Gly."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 12
    - (D) OTHER INFORMATION: /note= "Amino Acid 12 wherein Xaa is Ser or Arg."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 17
    - (D) OTHER INFORMATION: /note= "Amino Acid 17 wherein Xaa is Glu or Asp."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu Gln 1 5 15

Xaa

- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single

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(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /note= "Amino Acid 1 wherein Xaa is Glu or Asp."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 3
  - (D) OTHER INFORMATION: /note= "Amino Acid 3 wherein Xaa is Arg or Leu."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 10
  - (D) OTHER INFORMATION: /note= "Amino Acid 10 wherein Xaa is Glu or Gly."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 13
  - (D) OTHER INFORMATION: /note= "Amino Acid 13 wherein Xaa is Ser or Arg."
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu Glu 1 5 15

Gln

- (2) INFORMATION FOR SEQ ID NO:15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 2
    - (D) OTHER INFORMATION: /note= "Amino Acid 2 wherein Xaa is Glu or Asp."
  - (ix) FEATURE:

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- (A) NAME/KEY: Peptide
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Amino Acid 4 wherein Xaa is Arg or Leu."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 11
  - (D) OTHER INFORMATION: /note= "Amino Acid 11 wherein Xaa is Glu or Gly."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 14
  - (D) OTHER INFORMATION: /note= "Amino Acid 14 wherein Xaa is Ser or Arg."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa Asp Leu 1 5 10 15

Glu

- INFORMATION FOR SEQ ID NO:16:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 3
    - (D) OTHER INFORMATION: /note= "Amino Acid 3 wherein Xaa is Glu or Asp."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 5
    - (D) OTHER INFORMATION: /note= "Amino Acid 5 wherein Xaa is Arg or Leu."
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 12
    - (D) OTHER INFORMATION: /note= "Amino Acid 12 wherein Xaa is Glu or Gly."

- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 15
  - (D) OTHER INFORMATION: /note= "Amino Acid 15 wherein Xaa is Ser or Arg."
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa Asp 1 5 10 15

Leu

# ) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 4
  - (D) OTHER INFORMATION: /note= "Amino Acid 4 wherein Xaa is Glu or Asp."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 6
  - (D) OTHER INFORMATION: /note= "Amino Acid 6 wherein Xaa is Arg or Leu."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 13
  - (D) OTHER INFORMATION: /note= "Amino Acid 13 wherein Xaa is Glu or Gly."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 16
  - (D) OTHER INFORMATION: /note= "Amino Acid 16 wherein Xaa is Ser or Arg."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln Xaa 1 5 10 15

Asp

- (2) INFORMATION FOR SEQ ID NO:18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 5
    - (D) OTHER INFORMATION: /note= "Amino Acid 5 wherein Xaa is Glu or Asp."
  - (ix) FEATURE:

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- (A) NAME/KEY: Peptide
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /note= "Amino Acid 7 wherein Xaa is Arg or Leu."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 14
  - (D) OTHER INFORMATION: /note= "Amino Acid 14 wherein Xaa is Glu or Gly."
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 17
  - (D) OTHER INFORMATION: /note= "Amino Acid 17 wherein Xaa is Ser or Arg."
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp Leu Glu Gln Xaa Arg Xaa Ala Lys Glu Lys Leu Gln Xaa Gln Gln 1 5 15

Xaa

- (2) INFORMATION FOR SEQ ID NO:19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 107 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg Lys Lys Glu His Gly
1 10 15

Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu Glu Ile Pro Ala Ile 20 25 30

Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr Ile Pro His Gln Ser 35 40 45

Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg Asp Ser Lys Glu Ile 50 55 60

Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile Thr Thr Asn Val Glu 65 70 75 80

Gly Arg Arg Asp Ile His Lys Gly His Leu Glu Glu Lys Lys Asp Gly ,85 90 95

Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser 100 105

### INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 117 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Gln Glu Gln Arg Asp Leu Glu Gln Arg Lys Ala Asp Thr Lys
1 5 10 15

Lys Asn Leu Glu Arg Lys Lys Glu His Gly Asp Ile Leu Ala Glu Asp 20 25 30

Leu Tyr Gly Arg Leu Glu Ile Pro Ala Ile Glu Leu Pro Ser Glu Asn 35 40 45 Glu Arg Gly Tyr Tyr Ile Pro His Gln Ser Ser Leu Pro Gln Asp Asn 50 55 60

Arg Gly Asn Ser Arg Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr 65 70 75 80

Asn Arg Glu Ser Ile Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His 85 90 95

Lys Gly His Leu Glu Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln
100 105 110

Lys Glu Asp Lys Ser 115

# (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp Thr Lys Lys Asn Leu Glu Arg Lys Lys Glu His Gly Asp Ile Leu 1 5 10 15

Ala Glu Asp Leu Tyr Gly Arg Leu Glu Ile Pro 20 25

- (2) INFORMATION FOR SEQ ID NO:22:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 24 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
    - (x) PUBLICATION INFORMATION:
      - (H) DOCUMENT NUMBER: WO 92/13884
      - (J) PUBLICATION DATE: 20-AUG-1992
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Arg Asp Leu Glu 1 5 15

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Gln Arg Lys Ala Asp Thr Lys Lys 20

- (2) INFORMATION FOR SEQ ID NO:23:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 31 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
    - (x) PUBLICATION INFORMATION:
      - (H) DOCUMENT NUMBER: WO 92/13884
      - (J) PUBLICATION DATE: 20-AUG-1992
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asn Ser Arg Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg 1 10 15

Glu Ser Ile Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys
20 25 30

- (2) INFORMATION FOR SEQ ID NO:24:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 151 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
    - (x) PUBLICATION INFORMATION:
      - (H) DOCUMENT NUMBER: WO 92/13884
      - (J) PUBLICATION DATE: 20-AUG-1992
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Arg Asp Glu Leu Phe Asn Glu Leu Leu Asn Ser Val Asp Val Asn Gly 1 5 10 15

Glu Val Lys Glu Asn Ile Leu Glu Glu Ser Gln Val Asn Asp Asp Ile 20 25 30

Phe Asn Ser Leu Val Lys Ser Val Gln Gln Gln Gln His Asn Val
35 40 45

Glu Glu Lys Val Glu Glu Ser Val Glu Glu Asn Asp Glu Glu Ser Val
50 55 60

Glu Glu Asn Val Glu Glu Asn Val Glu Glu Asn Asp Asp Gly Ser Val 65 70 75 80

Ala Ser Ser Val Glu Glu Ser Ile Ala Ser Ser Val Asp Glu Ser Ile 85 90 95

Asp Ser Ser Ile Glu Glu Asn Val Ala Pro Thr Val Glu Glu Ile Val 100 105 110

Ala Pro Thr Val Glu Glu Ile Val Ala Pro Ser Val Val Glu Lys Cys 115 120 125

Ala Pro Ser Val Glu Glu Ser Val Ala Pro Ser Val Glu Glu Ser Val 130 135 140

Ala Glu Met Leu Lys Glu Arg 145 150

### (2) INFORMATION FOR SEQ ID NO:25:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Arg Asp Glu Leu Phe Asn Glu Leu Leu Asn Ser Val Asp Val Asn Gly
1 5 10 15

Glu Val Lys Glu Asn Ile Leu Glu Glu Ser Gln Val Asn Asp Asp Ile 20 25 30

Phe Asn Ser Leu Val Lys Ser Val Gln Gln Gln Gln Gln His Asn 35 40 45

### (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asp Glu Leu Phe Asn Glu Leu Leu Asn Ser Val Asp Val Asn Gly Glu 1 5 10 15

Val Lys Glu Asn Ile Leu Glu Glu Ser Gln 20 25

### (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Leu Glu Glu Ser Gln Val Asn Asp Asp Ile Phe Ser Asn Ser Leu Val
1 5 10 15

Lys Ser Val Gln Gln Gln Gln His Asn Val 20 25

## (2) INFORMATION FOR SEQ ID NO:28:

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- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Val Glu Lys Cys Ala Pro Ser Val Glu Glu Ser Val Ala Pro Ser Val 1 5 10 15

Glu Glu Ser Val Ala Glu Met Leu Lys Glu Arg 20 25

- (2) INFORMATION FOR SEQ ID NO:29:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

|  |          | (D) TOPOLOGY: linear   | -  |
|--|----------|--|----|
|  | (ii)     | MOLECULE TYPE: DNA (genomic)   |    |
|  | (x)      | PUBLICATION INFORMATION: (H) DOCUMENT NUMBER: WO 92/13884 (J) PUBLICATION DATE: 20-AUG-1992                                  |    |
|  | (xi)     | SEQUENCE DESCRIPTION: SEQ ID NO:29:  |    |
| TTG  | TTCTA    | A TCGCTTT  | 17 |
| (2)  | INFO     | MATION FOR SEQ ID NO:30:   |    |
|  | (i)      | SEQUENCE CHARACTERISTICS:  (A) LENGTH: 15 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear |    |
| The second secon | (ii)     | MOLECULE TYPE: DNA (genomic)   |    |
| The transfer of the transfer o | (x)      | PUBLICATION INFORMATION: (H) DOCUMENT NUMBER: WO 92/13884 (J) PUBLICATION DATE: 20-AUG-1992                                  |    |
|  | (xi)     | SEQUENCE DESCRIPTION: SEQ ID NO:30:  |    |
| AAAC   | AAGA     | A AATCT  | 15 |
| (2)  | INFO     | MATION FOR SEQ ID NO:31:   |    |
|  | (i)      | SEQUENCE CHARACTERISTICS:  (A) LENGTH: 316 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear |    |
| ,  | (ii)     | MOLECULE TYPE: peptide   |    |
|  | (x)      | PUBLICATION INFORMATION: (H) DOCUMENT NUMBER: WO 92/13884 (J) PUBLICATION DATE: 20-AUG-1992                                  |    |
|  | (xi)     | SEQUENCE DESCRIPTION: SEQ ID NO:31:  |    |
|  | Ser<br>1 | Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gl<br>5 10 15  | .n |
|  | Gln      | Ser Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu Lys Leu Gln Gl<br>20 25 30   | .u |
|  | Gln      | Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gl<br>35 40 45   | .n |

Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu 55 Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Ger Asp Leu Glu Gln Asp Arg Leu Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys 105 Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala 120 Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln Glu 165 Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Ser Asp Leu Glu Gln 180 185 Glu Arg Arg Ala Lys Glu Lys Leu Gln Glu Gln Gln Arg Asp Leu Glu 200 Gln Arg Lys Ala Asp Thr Lys Lys Asn Leu Glu Arg Lys Lys Glu His 210 215 Gly Asp Ile Leu Ala Glu Asp Leu Tyr Gly Arg Leu Glu Ile Pro Ala 230 235 Ile Glu Leu Pro Ser Glu Asn Glu Arg Gly Tyr Tyr Ile Pro His Gln 245 250 Ser Ser Leu Pro Gln Asp Asn Arg Gly Asn Ser Arg Asp Ser Lys Glu 260 265 Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile Thr Thr Asn Val 280 Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu Glu Lys Lys Asp 290 300 Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser 305 310 315

### (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 950 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| AAAGCGATCT      | AGAACAAGAG | AGACGTGCTA | AAGAAAAGTT | GCAAGAACAA | CAAAGCGATT | 60  |
|-----------------|------------|------------|------------|------------|------------|-----|
| TAGAACAAGA      | TAGACTTGCT | AAAGAAAAGT | TACAAGAGCA | GCAAAGCGAT | TTAGAACAAG | 120 |
| AGAGACTTGC      | TAAAGAAAAG | TTGCAAGAAC | AACAAAGCGA | TCTAGAACAA | GAGAGACGTG | 180 |
| CTAAAGAAAA      | GTTGCAAGAA | CAACAAAGCG | ATTTAGAACA | AGAGAGACGT | GCTAAAGAAA | 240 |
| AĞTTGCAAGA<br>□ | ACAACAAAGC | GATTTAGAAC | AAGATAGACT | TGCTAAAGAA | AAGTTACAAG | 300 |
| AGCAGCAAAG      | CGATTTAGAA | CAAGAGAGAC | GTGCTAAAGA | AAAGTTGCAA | GAACAACAAA | 360 |
| GCGATTTAGA      | ACAAGAGAGA | CGTGCTAAAG | AAAAGTTGCA | AGAACAACAA | AGCGATTTAG | 420 |
| AACAAGAGAG      | ACTTGCTAAA | GAAAAGTTGC | AAGAACAACA | AAGCGATTTA | GAACAAGAGA | 480 |
|                 | AGAAAAGTTG | CAAGAACAAC | AAAGCGATTT | AGAACAAGAG | AGACGTGCTA | 540 |
| AAGAAAAGTT      | GCAAGAACAA | CAAAGCGATT | TAGAACAAGA | GAGACGTGCT | AAAGAAAAGT | 600 |
| TGCAAGAGCA      | GCAAAGAGAT | TTAGAACAAA | GGAAGGCTGA | TACGAAAAA  | AATTTAGAAA | 660 |
| GAAAAAAGGA      | ACATGGAGAT | ATATTAGCAG | AGGATTTATA | TGGTCGTTTA | GAAATACCAG | 720 |
| CTATAGAACT      | TCCATCAGAA | AATGAACGTG | GATATTATAT | ACCACATCAA | TCTTCTTTAC | 780 |
| CTCAGGACAA      | CAGAGGGAAT | AGTAGAGATT | CCAAGGAAAT | АТСТАТААТА | GAAAAAACAA | 840 |
| ATAGAGAATC      | TATTACAACA | AATGTTGAAG | GACGAAGGGA | TATACATAAA | CGACATCTTG | 900 |
|                 | AGATGGTTCA |            |            |            |            | 950 |
|                 |            | -          |            |            |            |     |

- (2) INFORMATION FOR SEQ ID NO:33:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 464 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
    - (x) PUBLICATION INFORMATION:
      - (H) DOCUMENT NUMBER: WO 92/13884
      - (J) PUBLICATION DATE: 20-AUG-1992

| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:  |     |
|---|-----|
| GAATTCCGTG ATGAACTTTT TAATGAATTA TTAAATAGTG TAGATGTTAA TGGAGAAGTA   | 60  |
| AAAGAAAATA TTTTGGAGGA AAGTCAAGTT AATGACGATA TTTTTAATAG TTTAGTAAAA   | 120 |
| AGTGTTCAAC AAGAACAACA ACACAATGTT GAAGAAAAG TTGAAGAAAG TGTAGAAGAA  | 180 |
| AATGACGAAG AAAGTGTAGA AGAAAATGTA GAAGAAAATG TAGAAGAAAA TGACGACGGA   | 240 |
| AGTGTAGCCT CAAGTGTTGA AGAAAGTATA GCTTCAAGTG TTGATGAAAG TATAGATTCA   | 300 |
| AGTATTGAAG AAAATGTAGC TCCAACTGTT GAAGAAATCG TAGCTCCAAC TGTTGAAGAA   | 360 |
| ATTGTAGCTC CAAGTGTTGT AGAAAAGTGT GCTCCAAGTG TTGAAGAAAG TGTAGCTCCA   | 420 |
| AGTGTTGAAG AAAGTGTAGC TGAAATGTTG AAGGAAAGGA   | 464 |
| (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 988 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (x) PUBLICATION INFORMATION:  (H) DOCUMENT NUMBER: WO 92/13884  (J) PUBLICATION DATE: 20-AUG-1992  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34: |     |
| AAAGTATACA TCTTCCTTCT TTACTTCTTA AAATGAAACA TATTTTTTTTTT  | 60  |

AAAGTATACA TCTTCCTTCT TTACTTCTTA AAATGAAACA TATTTTGTAC ATATCATTTT 60 ACTTTATCCT TGTTAATTTA TTGATATTTC ATATAAATGG AAAGATAATA AAGAATTCTG 120 AAAAAGATGA AATCATAAAA TCTAACTTGA GAAGTGGTTC TTCAAATTCT AGGAATCGAA 180 TAAATGAGGA AAATCACGAG AAGAAACACG TTTTATCTCA TAATTCATAT GAGAAAACTA 240 AAAATAATGA AAATAATAAA TTTTTCGATA AGGATAAAGA GTTAACGATG TCTAATGTAA 300 AAAATGTGTC ACAAACAAAT TTCAAAAGTC TTTTAAGAAA TCTTGGTGTT TCAGAGAATA 360 TATTCCTTAA AGAAAATAAA TTAAATAAGG AAGGGAAATT AATTGAACAC ATAATAAATG 420 ATGATGACGA TAAAAAAAA TATATTAAAG GGCAAGACGA AAACAGACAA GAAGATCTTG 480 AAGAAAAAGC AGCTAAAGAA AAGTTACAGG GGCAACAAAG CGATTCAGAA CAAGAGAGAC 540 GTGCTAAAGA AAAGTTGCAA GAACAACAAA GCGATTTAGA ACAAGAGAGA CTTGCTAAAG 600 AAAAGTTGCA AGAACAACAA AGCGATTTAG AACAAGAGA ACGTGCTAAA GAAAAGTTGC 660

| AAG                  | AACAA  | ACA AAGCGATTTA GAACAAGAGA GACTTGCTAA AGAAAAGTTG   | CAAGAACAAC | 720 |
|----------------------|--------|---|------------|-----|
| AAA                  | GCGAT  | TT AGAACAAGAG AGACGTGCTA AAGAAAAGTT GCAAGAACAA  | CAAAGCGATT | 780 |
| TAG                  | AACAA  | GA GAGACGTGCT AAAGAAAAGT TGCAAGAACA ACAAAGCGAT  | TTAGAACAAG | 840 |
| AGA                  | GACTT  | GC TAAAGAAAG TTACAAGAGC AGCAAAGCGA TTTAGAACAA   | GATAGACTTG | 900 |
| CTA                  | AAGAA  | AA GTTGCAAGAA CAACAAAGCG ATTTAGAACA AGAGAGACGT  | GCTAAAGAAA | 960 |
| GGT                  | TGCAA  | GA ACAACAAAGC GATTTAGA  |            | 988 |
| (2)                  | INFO   | RMATION FOR SEQ ID NO:35:   |            |     |
|                      | (i)    | SEQUENCE CHARACTERISTICS:  (A) LENGTH: 12 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  |            |     |
|                      | (ii)   | MOLECULE TYPE: DNA (genomic)  |            |     |
| The traff the Hall H | (x)    | PUBLICATION INFORMATION: (H) DOCUMENT NUMBER: WO 92/13884 (J) PUBLICATION DATE: 20-AUG-1992                                   |            |     |
| 1                    | (xi)   | SEQUENCE DESCRIPTION: SEQ ID NO:35:   |            |     |
| AŢĠ                  | AAACA: | TA TT   |            | 12  |
| (2)                  | INFO   | RMATION FOR SEQ ID NO:36:   |            |     |
| g make               | (i)    | SEQUENCE CHARACTERISTICS:  (A) LENGTH: 12 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  | ·          |     |
|                      | (ii)   | MOLECULE TYPE: DNA (genomic)  | ,          |     |
|                      | (x)    | PUBLICATION INFORMATION: (H) DOCUMENT NUMBER: WO 92/13884 (J) PUBLICATION DATE: 20-AUG-1992                                   |            |     |
|                      | (xi)   | SEQUENCE DESCRIPTION: SEQ ID NO:36:   |            |     |
| AAG                  | CGATTT | TA GA   |            | 12  |
| (2)                  | INFOR  | RMATION FOR SEQ ID NO:37:   |            |     |
|                      | (i)    | SEQUENCE CHARACTERISTICS:  (A) LENGTH: 954 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear |            |     |

- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

  - (A) NAME/KEY: CDS
    (B) LOCATION: 1..954
- (x) PUBLICATION INFORMATION:
  - (H) DOCUMENT NUMBER: WO 92/13884
  - (J) PUBLICATION DATE: 20-AUG-1992
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| ATG<br>Met<br>1   | AAA<br>Lys        | CAT<br>His        | ATT               | TTG<br>Leu<br>5   | TAC<br>Tyr        | ATA<br>Ile        | TCA<br>Ser        | TTT<br>Phe        | TAC<br>Tyr<br>10  | Phe               | ATC<br>Ile        | CTT<br>Leu        | GTT<br>Val        | AAT<br>Asn<br>15  | TTA<br>Leu        | 4   | 8  |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|----|
| TTG<br>Leu<br>    | ATA<br>Ile        | TTT               | CAT<br>His<br>20  | ATA<br>Ile        | AAT<br>Asn        | GGA<br>Gly        | AAG<br>Lys        | ATA<br>Ile<br>25  | Ile               | AAG<br>Lys        | AAT<br>Asn        | TCT               | GAA<br>Glu<br>30  |                   | GAT<br>Asp        | 9   | 6  |
| €<br>GFĀ          | ATC<br>Ile        | ATA<br>Ile<br>35  | Lys               | TCT<br>Ser        | AAC<br>Asn        | TTG<br>Leu        | AGA<br>Arg<br>40  | AGT<br>Ser        | GGT<br>Gly        | TCT<br>Ser        | TCA<br>Ser        | AAT<br>Asn<br>45  | TCT<br>Ser        | AGG<br>Arg        | AAT<br>Asn        | 14  | 4  |
| CGA<br>Arg        | ATA<br>Ile<br>50  | AAT<br>Asn        | GAG<br>Glu        | GAA<br>Glu        | AAT<br>Asn        | CAC<br>His<br>55  | GAG<br>Glu        | AAG<br>Lys        | AAA<br>Lys        | CAC<br>His        | GTT<br>Val<br>60  | Leu               | TCT<br>Ser        | CAT<br>His        | AAT<br>Asn        | 19  | 2  |
| TCA<br>Ser<br>65  | TAT               | GAG<br>Glu        | AAA<br>Lys        | ACT<br>Thr        | AAA<br>Lys<br>70  | AAT<br>Asn        | AAT<br>Asn        | GAA<br>Glu        | AAT<br>Asn        | AAT<br>Asn<br>75  | AAA<br>Lys        | TTT<br>Phe        | TTC<br>Phe        | GAT<br>Asp        | AAG<br>Lys<br>80  | 24  | 0  |
| GĀT<br>Asp        | AAA<br>Lys        | GAG<br>Glu        | TTA<br>Leu        | ACG<br>Thr<br>85  | ATG<br>Met        | TCT<br>Ser        | AAT<br>Asn        | GTA<br>Val        | AAA<br>Lys<br>90  | AAT<br>Asn        | GTG<br>Val        | TCA<br>Ser        | CAA<br>Gln        | ACA<br>Thr<br>95  | AAT<br>Asn        | 28  | 8  |
| TTC<br>Phe        | AAA<br>Lys        | AGT<br>Ser        | CTT<br>Leu<br>100 | TTA<br>Leu        | AGA<br>Arg        | AAT<br>Asn        | CTT<br>Leu        | GGT<br>Gly<br>105 | GTT<br>Val        | TCA<br>Ser        | GAG<br>Glu        | AAT<br>Asn        | ATA<br>Ile<br>110 | TTC<br>Phe        | CTT<br>Leu        | 33  | 6  |
| AAA<br>Lys        | GAA<br>Glu        | AAT<br>Asn<br>115 | AAA<br>Lys        | TTA<br>Leu        | AAT<br>Asn        | AAG<br>Lys        | GAA<br>Glu<br>120 | GGG<br>Gly        | AAA<br>Lys        | TTA<br>Leu        | ATT<br>Ile        | GAA<br>Glu<br>125 | CAC<br>His        | ATA<br>Ile        | ATA<br>Ile        | 38  | 4  |
| AAT<br>Asn        | GAT<br>Asp<br>130 | GAT<br>Asp        | GAC<br>Asp        | GAT<br>Asp        | AAA<br>Lys        | AAA<br>Lys<br>135 | AAA<br>Lys        | TAT<br>Tyr        | ATT<br>Ile        | AAA<br>Lys        | GGG<br>Gly<br>140 | CAA<br>Gln        | GAC<br>Asp        | GAA<br>Glu        | AAC<br>Asn        | 43: | 2  |
| AGA<br>Arg<br>145 | CAA<br>Gln        | GAA<br>Glu        | GAT<br>Asp        | CTT<br>Leu        | GAA<br>Glu<br>150 | GAA<br>Glu        | AAA<br>Lys        | GCA<br>Ala        | GCT<br>Ala        | AAA<br>Lys<br>155 | GAA<br>Glu        | AAG<br>Lys        | TTA<br>Leu        | CAG<br>Gln        | GGG<br>Gly<br>160 | 480 | J. |
| CAA<br>Gln        | CAA<br>Gln        | AGC<br>Ser        | Asp               | TCA<br>Ser<br>165 | GAA<br>Glu        | CAA<br>Gln        | GAG<br>Glu        | Arg               | CGT<br>Arg<br>170 | GCT<br>Ala        | AAA<br>Lys        | GAA<br>Glu        | AAG<br>Lys        | TTG<br>Leu<br>175 | CAA<br>Gln        | 528 | 3  |

| GAA<br>Glu              | CAA<br>Gln        | CAA<br>Gln        | AGC<br>Ser<br>180                    | GAT<br>Asp          | TTA<br>Leu           | GAA<br>Glu         | CAA<br>Gln          | GAG<br>Glu<br>185 | Arg               | CTT<br>Leu        | GCT<br>Ala        | AAA<br>Lys        | GAA<br>Glu<br>190 | AAG<br>Lys        | TTG<br>Leu        |      | 576 |
|-------------------------|-------------------|-------------------|--------------------------------------|---------------------|----------------------|--------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|-----|
| CAA<br>Gln              | GAA<br>Glu        | CAA<br>Gln<br>195 | CAA<br>Gln                           | AGC                 | GAT<br>Asp           | TTA<br>Leu         | GAA<br>Glu<br>200   | Gln               | GAG<br>Glu        | AGA<br>Arg        | CGT<br>Arg        | GCT<br>Ala<br>205 | AAA<br>Lys        | GAA<br>Glu        | AAG<br>Lys        | is . | 624 |
| TTG<br>Leu              | CAA<br>Gln<br>210 | GAA<br>Glu        | CAA<br>Gln                           | CAA<br>Gln          | AGC<br>Ser           | GAT<br>Asp<br>215  | TTA                 | GAA<br>Glu        | CAA<br>Gln        | GAG<br>Glu        | AGA<br>Arg<br>220 | CTT<br>Leu        | GCT<br>Ala        | AAA<br>Lys        | GAA<br>Glu        |      | 672 |
| AAG<br>Lys<br>225       | TTG<br>Leu        | CAA<br>Gln        | GAA<br>Glu                           | CAA<br>Gln          | CAA<br>Gln<br>230    | AGC<br>Ser         | GAT<br>Asp          | TTA<br>Leu        | GAA<br>Glu        | CAA<br>Gln<br>235 | GAG<br>Glu        | AGA<br>Arg        | CGT<br>Arg        | GCT<br>Ala        | AAA<br>Lys<br>240 |      | 720 |
| GAA<br>GILu<br>LI<br>LI | AAG<br>Lys        | TTG<br>Leu        | CAA<br>Gln                           | GAA<br>Glu<br>245   | CAA<br>Gln           | CAA<br>Gln         | AGC<br>Ser          | GAT<br>Asp        | TTA<br>Leu<br>250 | GAA<br>Glu        | CAA<br>Gln        | GAG<br>Glu        | AGA<br>Arg        | CGT<br>Arg<br>255 | GCT<br>Ala        |      | 768 |
| ינו<br>סי<br>פאר        | GIU               | гуs               | 260                                  | GIN                 | Glu                  | Gln                | Gln                 | Ser<br>265        | GAT<br>Asp        | Leu               | Glu               | Gln               | Glu<br>270        | Arg               | Leu               |      | 816 |
| Lia<br>Lia              | тур               | 275               | гÀг                                  | Leu                 | GIN                  | GIu                | GIn<br>280          | Gln               | AGC<br>Ser        | Asp               | Leu               | Glu<br>285        | Gln               | Asp               | Arg               |      | 864 |
| ned                     | GCT<br>Ala<br>290 | AAA<br>Lys        | GAA<br>Glu                           | AAG<br>Lys          | TTG<br>Leu           | CAA<br>Gln<br>295  | GAA<br>Glu          | CAA<br>Gln        | CAA<br>Gln        | AGC<br>Ser        | GAT<br>Asp<br>300 | TTA<br>Leu        | GAA<br>Glu        | CAA<br>Gln        | GAG<br>Glu        |      | 912 |
| AGĀ<br>Arg<br>305       | CGT<br>Arg        | GCT<br>Ala        | AAA<br>Lys<br>—                      | GAA<br>Glu          | AGG<br>Arg<br>310    | TTG<br>Leu         | CAA<br>Gln          | GAA<br>Glu        | CAA<br>Gln        | CAA<br>Gln<br>315 | AGC<br>Ser        | GAT<br>Asp        | TTA<br>Leu        |                   |                   | •    | 954 |
| (2)                     | INFO              | RMAT              | ION                                  | FOR                 | SEQ                  | ID N               | 0:38                | :                 |                   | •                 | -                 |                   |                   |                   |                   |      |     |
|                         | (i)               | (A<br>(B<br>(C    | UENC<br>) LE<br>) TY<br>) ST<br>) TO | NGTH<br>PE:<br>RAND | : 14<br>nucl<br>EDNE | 93 b<br>eic<br>SS: | ase<br>acid<br>sing | pair              | 's                |                   |                   |                   |                   |                   | ٠                 |      | ٠,  |
|                         | (ii)              | MOL               | ECUL                                 | Е ТҮ                | PE:                  | DNA                | (gen                | omic              | )                 |                   |                   |                   |                   |                   |                   |      |     |
|                         | (x)               | (H                | LICA'<br>) DO<br>) PU                | CUME:               | NT N                 | UMBE:              | R: W                | 0 92              | /138<br>UG-1      | 84<br>992         |                   | ,                 |                   |                   |                   |      |     |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CAAGAACAAC AAAGCGATCT AGAACAAGAG AGACGTGCTA AAGAAAAGTT GCAAGAACAA

CAAAGCGATT TAGAACAAGA TAGACTTGCT AAAGAAAAGT TACAAGAGCA GCAAAGCGAT

60

120

| TTAGAACAAG       | AGAGACTTGC | TAAGAAAAGT | TGCAAGAACA | ACAAAGCGAT | CTAGAACAAG | . 180 |
|------------------|------------|------------|------------|------------|------------|-------|
| AGAGACGTGC       | TAAAGAAAAG | TTGCAAGAAC | AACAAAGCGA | TTTAGAACAA | GAGAGACGTG | 240   |
| CTAAAGAAAA       | GTTGCAAGAA | CAACAAAGCG | ATTTAGAACA | AGATAGACTT | GCTAAAGAAA | 300   |
| AGTTACAAGA       | GCAGCAAAGC | GATTTAGAAC | AAGAGAGACG | TGCTAAAGAA | AAGTTGCAAG | 360   |
| AACAACAAAG       | CGATTTAGAA | CAAGAGAGAC | GTGCTAAGAA | AAGTTGCAAG | AACAACAAAG | 420   |
| CGATTTAGAA       | CAAGAGAGAC | TTGCTAAAGA | AAAGTTGCAA | GAACAACAAA | GCGATTTAGA | 480   |
| ACAAGAGAGA       | CGTGCTAAAG | AAAAGTTGCA | AGAACAACAA | AGCGATTTAG | AACAAGAGAG | 540   |
| ACGTGCTAAG       | AAAAGTTGCA | AGAACAACAA | AGCGATTTAG | AACAAGAGAG | ACGTGCTAAA | 600   |
| GAAAAGTTGC       | AAGAGCAGCA | AAGAGATTTA | GAACAAAGGA | AGGCTGATAC | GAAAAAAAAT | 660   |
| TTĀGAAAGAA<br>∖∐ | AAAAGGAACA | TGGAGATATA | TTAGCAGAGG | ATTTATATGG | TCGTTTAGAA | 720   |
| ATACCAGCTA       | TAGAACTTCC | ATCAGAAAAT | GAACGTGGAT | ATTATATACC | ACATCAATCT | 780   |
| TCTTTACCTC       | AGGACAACAG | AGGGAATAGT | AGAGATTCCA | AGGAAATATC | TATAATAGAA | . 840 |
| AAAACAAATA       | GAGAATCTAT | TACAACAAAT | GTTGAAGGAC | GAAGGGATAT | ACATAAAGGA | 900   |
| CATCTTGAAG       | AAAAGAAAGA | TGGTTCAATA | AAACCAGAAC | AAAAAGAAGA | TAAATCTGCT | 960   |
| GACATACAAA       | ATCATACATT | AGAGACAGTA | AATATTTCTG | ATGTTAATGA | TTTTCAAATA | 1020  |
| AGTAAGTATG       | AGGATGAAAT | AAGTGCTGAA | TATGACGATT | CATTAATAGA | TGAAGAAGAA | 1080  |
| GÄTGATGAAG       | ACTTAGACGA | ATTTAAGCCT | ATTGTGCAAT | ATGACAATTT | CCAAGATGAA | 1140  |
| GAAAACATAG       | GAAŢTTATAA | AGAACTAGAA | GATTTGATAG | AGAAAAATGA | AAATTTAGAT | 1200  |
| GATTTAGATG       | AAGGAATAGA | AAAATCATCA | GAAGAATTAT | CTGAAGAAAA | AATAAAAAA  | 1260  |
| GGAAAGAAAT       | ATGAAAAAAC | AAAGGATAAT | AATTTTAAAC | CAAATGATAA | AAGTTTGTAT | 1320  |
| GATGAGCATA       | ТТААААААТА | TAAAAATGAT | AAGCAGGTTA | ATAAGGAAAA | GGAAAAATTC | 1380  |
| ATAAAATCAT       | TGTTTCATAT | ATTTGACGGA | GACAATGAAA | TTTTACAGAT | CGTGGATGAG | 1440  |
| TTATCTGAAG       | АТАТААСТАА | ATATTTTATG | АААСТАТААА | AGGTTATATA | TTT        | 1493  |
|                  |            |            |            |            |            |       |

# (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs

  - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

|  | (x)   | PUBLIC<br>(H) D<br>(J) P    | ATION II<br>OCUMENT<br>UBLICAT                           | NUMBER                        | R: WO                  | 92/1<br>-AUG     | 3884<br>-199: | 2             |            |                  |                  |            | ٠   |     |
|--|-------|-----------------------------|--|-------------------------------|------------------------|------------------|---------------|---------------|------------|------------------|------------------|------------|-----|-----|
|  | (xi)  | SEQUEN                      | CE DESCI   | RIPTION                       | : SEQ                  | ID 1             | NO:39         | 9:            |            |                  |                  |            |     |     |
| CAA  | GAAC  | AC AA                       |  |                               |                        |                  | -             |               |            |                  |                  |            | - % | 12  |
| (2)  | INFO  | RMATION                     | FOR SEG  | ON DI O                       | :40:                   |                  |               |               |            |                  |                  |            |     |     |
|  | (i)   | (B) T<br>(C) S              | CE CHARA<br>ENGTH: 1<br>YPE: nuc<br>TRANDEDN<br>OPOLOGY: | l2 base<br>cleic a<br>TESS: s | pair<br>cid<br>single  | S                |               |               |            |                  |                  |            |     |     |
|  | (ii)  | MOLECU                      | LE TYPE:   | DNA (                         | genom                  | ic)              |               |               |            |                  | -                |            |     |     |
|  | (x)   | PUBLICA<br>(H) DO<br>(J) PU | ATION IN<br>CUMENT<br>JBLICATI                           | NUMBER                        | : WO 9                 | 92/13<br>-AUG-   | 3884<br>-1992 | -<br><b>?</b> |            |                  |                  |            |     |     |
| 1000                                       | (xi)  | SEQUENC                     | CE DESCR   | RIPTION                       | : SEQ                  | ID N             | 10:40         | ):            |            |                  |                  |            |     |     |
| GGT'                                       | TATAT | AT TT                       |  |                               |                        | ٠                |               |               |            |                  |                  |            |     | 12  |
| (2)  | INFO  | RMATION                     | FOR SEQ  | ID NO                         | :41:                   |                  |               |               |            |                  |                  |            |     |     |
| The same same same same same same same sam | (i)   | (B) TY<br>(C) SI            | CE CHARA<br>INGTH: 1<br>PE: nuc<br>TRANDEDN<br>POLOGY:   | 482 ba<br>leic a<br>ESS: s    | se pai<br>cid<br>ingle | irs              |               |               |            |                  |                  |            |     |     |
|  | (ii)  | MOLECUI                     | E TYPE:  | DNA (                         | genomi                 | ic)              |               |               |            |                  |                  | •          |     |     |
|  | (ix)  | FEATURE<br>(A) NA<br>(B) LC | :<br>ME/KEY:<br>CATION:                                  | CDS<br>114                    | 82                     |                  |               |               |            |                  |                  |            |     |     |
|  | (x)   | PUBLICA<br>(H) DO<br>(J) PU | TION IN:<br>CUMENT :<br>BLICATION                        | NUMBER                        | : WO 9                 | 2/13<br>AUG-     | 884<br>1992   |               |            |                  |                  |            |     |     |
|  | (xi)  | SEQUENC                     | E DESCR  | IPTION                        | : SEQ                  | ID N             | 0:41          | :             |            |                  |                  |            |     |     |
| CAA<br>Gln<br>1                            | GAA ( | CAA CAA<br>Gln Gln          | AGC GAT<br>Ser Asp<br>5                                  | CTA GA                        | AA CAA<br>lu Gln       | GAG<br>Glu<br>10 | Arg           | CGT<br>Arg    | GCT<br>Ala | AAA<br>Lys       | GAA<br>Glu<br>15 | AAG<br>Lys |     | 48  |
| TTG<br>Leu                                 | CAA G | GAA CAA<br>Glu Gln<br>20    | CAA AGC<br>Gln Ser                                       | GAT TI<br>Asp Le              | A GAA<br>u Glu<br>25   | Gln              | GAT<br>Asp    | AGA<br>Arg    | CTT<br>Leu | GCT<br>Ala<br>30 | AAA<br>Lys       | GAA<br>Glu |     | 96  |
| AAG<br>Lys                                 | TTA C | AA GAG (                    | CAG CAA<br>Gln Gln                                       | AGC GA                        | T TTA<br>sp Leu        | GAA<br>Glu       | CAA<br>Gln    | GAG<br>Glu    | AGA<br>Arg | CTT<br>Leu       | GĆT<br>Ala       | AAA<br>Lys |     | 144 |

35 40 45

|                       |                  |                   |                   |                   |                   |                      | 4 (               | ,                 |                   |                   |                   | 45                | •                 |                   |                    |     |
|-----------------------|------------------|-------------------|-------------------|-------------------|-------------------|----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-----|
| GAA<br>Glu            | AAG<br>Lys<br>50 | TTG<br>Leu        | CAA<br>Gln        | GAA<br>Glu        | A CAA             | A CAA<br>n Glr<br>55 | Ser               | C GAT             | CTA<br>Leu        | GAA<br>Glu        | CAA<br>Glr<br>60  | ı Glu             | AGA<br>Arg        | CGI<br>Ar         | GCT<br>Ala         | 192 |
| AAA<br>Lys<br>65      | GAA<br>Glu       | AAG<br>Lys        | _TTG<br>Leu       | CAA<br>Glr        | GAA<br>Glu<br>70  | ı Gln                | CAA<br>Glr        | AGC<br>Ser        | GAT<br>Asp        | TTA<br>Leu<br>75  | ı Glu             | CAA<br>Gln        | GAG<br>Glu        | ĀGA<br>Arg        | CGT<br>J Arg<br>80 | 240 |
| GCT<br>Ala            | AAA<br>Lys       | GAA<br>Glu        | AAG<br>Lys        | TTG<br>Leu<br>85  | GIN               | GAA<br>Glu           | CAA<br>Gln        | CAA<br>Glr        | AGC<br>Ser<br>90  | ' Asp             | TTA<br>Leu        | GAA<br>Glu        | CAA<br>Gln        | GAT<br>Asp        | AGA<br>Arg         | 288 |
|                       | nia              | гуз               | 100               | гÀг               | Leu               | Gin                  | Glu               | 105               | Gln               | Ser               | Asp               | Leu               | Glu<br>110        | Gln               | GAG<br>Glu         | 336 |
|                       | ary              | 115               | гуѕ               | GIU               | ьys               | Leu                  | 120               | GLu               | Gln               | Gln               | Ser               | 125               | Leu               | Glu               | CAA<br>Gln         | 384 |
| ii .                  | 130              | Arg               | AIA               | ьуs               | GIU               | Lys<br>135           | Leu               | Gln               | Glu               | Gln               | Gln<br>140        | Ser               | Asp               | Leu               | Glu                | 432 |
| CAA (Glh (            | JIU              | ALG               | Leu               | Ата               | 150               | GIU                  | rys               | Leu               | Gln               | Glu<br>155        | Gln               | Gln               | Ser               | Asp               | Leu<br>160         | 480 |
| GAA (                 | CAA<br>Sln       | GAG<br>Glu        | AGA<br>Arg        | CGT<br>Arg<br>165 | GCT<br>Ala        | AAA<br>Lys           | GAA<br>Glu        | AAG<br>Lys        | TTG<br>Leu<br>170 | CAA<br>Gln        | GAA<br>Glu        | CAA<br>Gln        | CAA<br>Gln        | AGC<br>Ser<br>175 | GAT<br>Asp         | 528 |
| TTA C                 | SAA<br>Slu       | CAA<br>Gln        | GAG<br>Glu<br>180 | AGA<br>Arg        | CGT<br>Arg        | GCT<br>Ala           | AAA<br>Lys        | GAA<br>Glu<br>185 | Lys               | TTG<br>Leu        | CAA<br>Gln        | GAA<br>Glu        | CAA<br>Gln<br>190 | CAA<br>Gln        | AGC<br>Ser         | 576 |
| GAT I<br>Asp L        | eu '             | GAA<br>Glu<br>195 | CAA<br>Gln        | GAG<br>Glu        | AGA<br>Arg        | CGT<br>Arg           | GCT<br>Ala<br>200 | AAA<br>Lys        | GAA<br>Glu        | AAG<br>Lys        | TTG<br>Leu        | CAA<br>Gln<br>205 | GAG<br>Glu        | CAG<br>Gln        | CAA<br>Gln         | 624 |
| AGA G<br>Arg A<br>2   | AT Sp            | TTA<br>Leu        | GAA<br>Glu        | CAA<br>Gln        | AGG<br>Arg        | AAG<br>Lys<br>215    | GCT<br>Ala        | GAT<br>Asp        | ACG<br>Thr        | AAA<br>Lys        | AAA<br>Lys<br>220 | AAT<br>Asn        | TTA<br>Leu        | GAA<br>Glu        | AGA<br>Arg         | 672 |
| AAA A<br>Lys L<br>225 | AG (             | GAA<br>Glu        | CAT<br>His        | GGA<br>Gly        | GAT<br>Asp<br>230 | ATA<br>Ile           | TTA<br>Leu        | GCA<br>Ala        | GAG<br>Glu        | GAT<br>Asp<br>235 | TTA<br>Leu        | TAT<br>Tyr        | GGT<br>Gly        | CGT<br>Arg        | TTA<br>Leu<br>240  | 720 |
| GAA A'<br>G u I       | TA (             | CCA (             | нта               | ATA<br>Ile<br>245 | GAA<br>Glu        | CTT<br>Leu           | CCA<br>Pro        | Ser               | GAA<br>Glu<br>250 | AAT<br>Asn        | GAA<br>Glu        | CGT<br>Arg        | GGA<br>Gly        | TAT<br>Tyr<br>255 | TAT<br>Tyr         | 768 |
| ATA CO                | CA C             | CAT (<br>His (    | CAA '             | TCT<br>Ser        | TCT<br>Ser        | TTA (<br>Leu         | CCT<br>Pro        | CAG<br>Gln        | GAC Asp           | AAC .<br>Asn      | AGA<br>Arg        | GGG :             | AAT .<br>Asn      | AGT<br>Ser        | AGA<br>Arg         | 816 |

260 265 270 GAT TCC AAG GAA ATA TCT ATA ATA GAA AAA ACA AAT AGA GAA TCT ATT 864 Asp Ser Lys Glu Ile Ser Ile Ile Glu Lys Thr Asn Arg Glu Ser Ile 275 ACA ACA AAT GTT GAA GGA CGA AGG GAT ATA CAT AAA GGA CAT CTT GAA 912 Thr Thr Asn Val Glu Gly Arg Arg Asp Ile His Lys Gly His Leu Glu 295 GAA AAG AAA GAT GGT TCA ATA AAA CCA GAA CAA AAA GAA GAT AAA TCT 960 Glu Lys Lys Asp Gly Ser Ile Lys Pro Glu Gln Lys Glu Asp Lys Ser 310 315 GCT GAC ATA CAA AAT CAT ACA TTA GAG ACA GTA AAT ATT TCT GAT GTT 1008 Ala Asp Ile Gln Asn His Thr Leu Glu Thr Val Asn Ile Ser Asp Val 325 330 AAT GAT TTT CAA ATA AGT AAG TAT GAG GAT GAA ATA AGT GCT GAA TAT 1056 Asn Asp Phe Gln Ile Ser Lys Tyr Glu Asp Glu Ile Ser Ala Glu Tyr 340 GAC GAT TCA TTA ATA GAT GAA GAA GAA GAT GAT GAA GAC TTA GAC GAA 1104 Asp Asp Ser Leu Ile Asp Glu Glu Glu Asp Asp Glu Asp Leu Asp Glu 355 TIT AAG CCT ATT GTG CAA TAT GAC AAT TTC CAA GAT GAA GAA AAC ATA 1152 Phe Lys Pro Ile Val Gln Tyr Asp Asn Phe Gln Asp Glu Glu Asn Ile 370 375 a£. GGA ATT TAT AAA GAA CTA GAA GAT TTG ATA GAG AAA AAT GAA AAT TTA 1200 Gly Ile Tyr Lys Glu Leu Glu Asp Leu Ile Glu Lys Asn Glu Asn Leu 385 390 395 GAT GAT TTA GAT GAA GGA ATA GAA AAA TCA TCA GAA GAA TTA TCT GAA 1248 Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu 405 1296 Glu Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn 420 TTT AAA CCA AAT GAT AAA AGT TTG TAT GAT GAG CAT ATT AAA AAA TAT 1344 Phe Lys Pro Asn Asp Lys Ser Leu Tyr Asp Glu His Ile Lys Lys Tyr 435 AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA TTC ATA AAA TCA 1392 Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser 450 TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT 1440 Leu Phe His Ile Phe Asp Gly Asp Asn Glu Ile Leu Gln Ile Val Asp 465 470 475 480 GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA 1482 Glu Leu Ser Glu Asp Ile Thr Lys Tyr Phe Met Lys Leu

|      |                        | 405 490  | •   |
|------|------------------------|--|-----|
| (2)  | INFORMA                | TION FOR SEQ ID NO:42:   |     |
| -    | ~ ()<br>. ()           | QUENCE CHARACTERISTICS: A) LENGTH: 12 base pairs B) TYPE: nucleic acid C) STRANDEDNESS: single D) TOPOLOGY: linear   | ,±. |
|      | (ii) MO                | LECULE TYPE: DNA (genomic)   |     |
| -    |                        | ATURE:<br>A) NAME/KEY: CDS<br>B) LOCATION: 112   |     |
|      | (1                     | BLICATION INFORMATION:<br>H) DOCUMENT NUMBER: WO 92/13884<br>J) PUBLICATION DATE: 20-AUG-1992  |     |
|      | (xi) SE                | QUENCE DESCRIPTION: SEQ ID NO:42:  |     |
| AAG  | GTT ATA<br>Val Ile     | , and the state of | 12  |
| (2-) | INFORMA                | TION FOR SEQ ID NO:43:   |     |
|      | ( <i>1</i><br>(1<br>(0 | QUENCE CHARACTERISTICS:<br>A) LENGTH: 12 base pairs<br>B) TYPE: nucleic acid<br>C) STRANDEDNESS: single<br>D) TOPOLOGY: linear   |     |
|      | (ii) MOI               | LECULE TYPE: DNA (genomic)   |     |
|      | (I                     | BLICATION INFORMATION:<br>H) DOCUMENT NUMBER: WO 92/13884<br>J) PUBLICATION DATE: 20-AUG-1992  |     |
|      | (xi) SEQ               | QUENCE DESCRIPTION: SEQ ID NO:43:  |     |
| CAAG | AACAAC A               | AA   | 12  |
| (2)  | INFORMAT               | TION FOR SEQ ID NO:44:   |     |
|      | ( <i>P</i><br>(E       | QUENCE CHARACTERISTICS:<br>A) LENGTH: 12 base pairs<br>B) TYPE: nucleic acid<br>C) STRANDEDNESS: single<br>D) TOPOLOGY: linear   |     |
|      | (ii) MOT               | FCULF TVDF. DNA (gonomia)  |     |

(x) PUBLICATION INFORMATION:
(H) DOCUMENT NUMBER: WO 92/13884

|                     |                  | 1                | (J) 1                   | PUBLI                           | CAT                 | ON I                | DATE:                | 20-               | -AUG-            | -1992            | 2                |                  |                   |                  |                  | •   |
|---------------------|------------------|------------------|-------------------------|---------------------------------|---------------------|---------------------|----------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|-----|
|                     | (xi              | i) si            | EQUE                    | CE I                            | ESCF                | RIPTI               | ON:                  | SEQ               | ID N             | NO:44            | <b>!</b> :       |                  |                   |                  |                  |     |
| ATG                 | AAAC             | TAT              | AA                      |                                 |                     |                     |                      |                   |                  |                  |                  |                  |                   |                  |                  | 12  |
| (2)                 | INE              | ORM              | OITA                    | , FOF                           | SEC                 | ) ID                | NO:4                 | 15:               |                  |                  | •                | _                |                   |                  |                  |     |
| ·                   |                  | .) SI<br>(       | EQUEN<br>(A) I<br>(B) I | ICE C<br>LENGT<br>LYPE:<br>TRAN | HARA<br>H: 1<br>nuc | CTEF<br>482<br>leic | RISTI<br>base<br>aci | CS:<br>pai        | irs              |                  |                  |                  |                   |                  |                  |     |
|                     | (ii              | ) MC             | LECU                    | LE T                            | YPE:                | DNA                 | (ge                  | nomi              | .c)              | •                |                  |                  |                   |                  |                  |     |
|                     | ·                | (                | B) I                    | E:<br>AME/<br>OCAT<br>ATIO      | ION:                | 1                   | 1482                 |                   |                  |                  |                  |                  |                   |                  |                  |     |
|                     |                  | (                | H) D                    | OCUM<br>UBLI                    | ${	t ENT}$          | NUMB                | ER:                  | WO 9              | 2/13<br>AUG-     | 884              |                  |                  |                   |                  |                  |     |
|                     | (xi              |                  |                         | CE D                            |                     |                     |                      |                   |                  |                  |                  |                  |                   |                  |                  |     |
| ( <del>)</del>      |                  |                  |                         |                                 |                     |                     |                      |                   |                  |                  |                  |                  |                   |                  |                  |     |
| Glin                | Glu              | Gln              | Gln                     | AGC<br>Ser<br>5                 | Asp                 | Leu                 | GAA                  | Gln               | GAG<br>Glu<br>10 | Arg              | Arg              | GCT<br>Ala       | AAA<br>Lys        | GAA<br>Glu<br>15 | Lys              | 48  |
| T <b>T</b> G<br>Leu | CAA<br>Gln       | GAA<br>Glu       | CAA<br>Gln<br>20        | CAA<br>Gln                      | AGC<br>Ser          | GAT<br>Asp          | TTA<br>Leu           | GAA<br>Glu<br>25  | Gln              | GAT<br>Asp       | AGA<br>Arg       | CTT<br>Leu       | GCT<br>Ala<br>30  | Lys              | GAA<br>Glu       | 96  |
| AAG<br>Lys          | TTA<br>Leu       | CAA<br>Gln<br>35 | GAG<br>Glü              | CAG<br>Gln                      | CAA<br>Gln          | AGC<br>Ser          | GAT<br>Asp<br>40     | TTA<br>Leu        | GAA<br>Glu       | CAA<br>Gln       | GAG<br>Glu       | AGA<br>Arg<br>45 | CTT<br>Leu        | GCT<br>Ala       | AAA<br>Lys       | 144 |
| GAA<br>Glu          | AAG<br>Lys<br>50 | TTG<br>Leu       | CAA<br>Gln              | GAA<br>Glu                      | CAA<br>Gln          | CAA<br>Gln<br>55    | AGC<br>Ser           | GAT<br>Asp        | CTA<br>Leu       | GAA<br>Glu       | CAA<br>Gln<br>60 | GAG<br>Glu       | AGA<br>Arg        | CGT<br>Arg       | GCT<br>Ala       | 192 |
| AAA<br>Lys<br>65    | GAA<br>Glu       | AAG<br>Lys       | TTG<br>Leu              | CAA<br>Gln                      | GAA<br>Glu<br>70    | CAA<br>Gln          | CAA<br>Gln           | AGC<br>Ser        | GAT<br>Asp       | TTA<br>Leu<br>75 | GAA<br>Glu       | CAA<br>Gln       | GAG<br>Glu        | AGA<br>Arg       | CGT<br>Arg<br>80 | 240 |
| GCT<br>Ala          | AAA<br>Lys       | GAA<br>Glu       | AAG<br>Lys              | TTG<br>Leu<br>85                | CAA<br>Gln          | GAA<br>Glu          | CAA<br>Gln           | CAA<br>Gln        | AGC<br>Ser<br>90 | GAT<br>Asp       | TTA<br>Leu       | GAA<br>Glu       | CAA<br>Gln        | GAT<br>Asp<br>95 | AGA<br>Arg       | 288 |
| CTT<br>Leu          | GCT<br>Ala       | AAA<br>Lys       | GAA<br>Glu<br>100       | AAG<br>Lys                      | TTA<br>Leu          | CAA<br>Gln          | GAG<br>Glu           | CAG<br>Gln<br>105 | CAA<br>Gln       | AGC<br>Ser       | GAT<br>Asp       | TTA<br>Leu       | GAA<br>Glu<br>110 | CAA<br>Gln       | GAG<br>Glu       | 336 |
| AGA<br>Arg          | CGT<br>Arg       | GCT<br>Ala       | AAA<br>Lys              | GAA<br>Glu                      | AAG<br>Lys          | TTG<br>Leu          | CAA<br>Gln           | GAA<br>Glu        | CAA<br>Gln       | CAA<br>Gln       | AGC<br>Ser       | GAT<br>Asp       | TTA<br>Leu        | GAA<br>Glu       | CAA<br>Gln       | 384 |

|                   |                   | 115               |                   |                   |                   |                   | 120               |                   |                   | ~                 |                   | 125               |                   |                   |                   |          |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----------|
|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   | AGC               |                   |                   | GAA<br>Glu        | 432      |
| CAA<br>Gln<br>145 | GAG<br>Glu        | AGA<br>Arg        | CTT<br>Leu        | GCT<br>Ala        | AAA<br>Lys<br>150 | GAA<br>Glu        | AAG<br>Lys        | TTG<br>Leu        | CAA<br>Gln        | GAA<br>Glu<br>155 | CAA<br>Gln        | CAA<br>Gln        | AGC<br>Ser        | GAT<br>Asp        | TTA<br>Leu<br>160 | 480      |
| GAA<br>Glu        | CAA<br>Gln        | GAG<br>Glu        | AGA<br>Arg        | CGT<br>Arg<br>165 | GCT<br>Ala        | AAA<br>Lys        | GAA<br>Glu        | AAG<br>Lys        | TTG<br>Leu<br>170 | CAA<br>Gln        | GAA<br>Glu        | CAA<br>Gln        | CAA<br>Gln        | AGC<br>Ser<br>175 | GAT<br>Asp        | 528<br>· |
| TTA<br>Leu        | GAA<br>Glu        | CAA<br>Gln        | GAG<br>Glu<br>180 | AGA<br>Arg        | CGT<br>Arg        | GCT<br>Ala        | AAA<br>Lys        | GAA<br>Glu<br>185 | AAG<br>Lys        | TTG<br>Leu        | CAA<br>Gln        | GAA<br>Glu        | CAA<br>Gln<br>190 | CAA<br>Gln        | AGC<br>Ser        | 576      |
| GAT               | TTA<br>Leu        | GAA<br>Glu<br>195 | CAA<br>Gln        | GAG<br>Glu        | AGA<br>Arg        | CGT<br>Arg        | GCT<br>Ala<br>200 | AAA<br>Lys        | GAA<br>Glu        | AAG<br>Lys        | TTG<br>Leu        | CAA<br>Gln<br>205 | GAG<br>Glu        | CAG<br>Gln        | CAA<br>Gln        | 624      |
| Arg               | GAT<br>Asp<br>210 | TTA<br>Leu        | GAA<br>Glu        | CAA<br>Gln        | AGG<br>Arg        | AAG<br>Lys<br>215 | GCT<br>Ala        | GAT<br>Asp        | ACG<br>Thr        | AAA<br>Lys        | AAA<br>Lys<br>220 | AAT<br>Asn        | TTA<br>Leu        | GAA<br>Glu        | AGA<br>Arg        | 672      |
| AAA<br>Lys<br>225 | AAG<br>Lys        | GAA<br>Glu        | CAT<br>His        | GGA<br>Gly        | GAT<br>Asp<br>230 | ATA<br>Ile        | TTA<br>Leu        | GCA<br>Ala        | GAG<br>Glu        | GAT<br>Asp<br>235 | TTA<br>Leu        | TAT<br>Tyr        | GGT<br>Gly        | CGT<br>Arg        | TTA<br>Leu<br>240 | 720      |
| GAA<br>Glu        | ATA<br>Ile        | CCA<br>Pro        | GCT<br>Ala        | ATA<br>Ile<br>245 | GAA<br>Glu        | CTT<br>Leu        | CCA<br>Pro        | TCA<br>Ser        | GAA<br>Glu<br>250 | AAT<br>Asn        | GAA<br>Glu        | CGT<br>Arg        | GGA<br>Gly        | TAT<br>Tyr<br>255 | TAT<br>Tyr        | 768      |
| ATA<br>Ile        | CCA<br>Pro        | CAT<br>His        | CAA<br>Gln<br>260 | TCT<br>Ser        | TCT<br>Ser        | TTA<br>Leu        | CCT<br>Pro        | CAG<br>Gln<br>265 | GAC<br>Asp        | AAC<br>Asn        | AGA<br>Arg        | GGG<br>Gly        | AAT<br>Asn<br>270 | AGT<br>Ser        | AGA<br>Arg        | 816      |
| GAT<br>Asp        | TCC<br>Ser        | AAG<br>Lys<br>275 | GAA<br>Glu        | ATG<br>Met        | TCT<br>Ser        | ATA<br>Ile        | ATA<br>Ile<br>280 | GAA<br>Glu        | AAA<br>Lys        | ACA<br>Thr        | AAT<br>Asn        | AGA<br>Arg<br>285 | GAA<br>Glu        | TCT<br>Ser        | ATT<br>Ile        | 864      |
| ACA<br>Thr        | ACA<br>Thr<br>290 | AAT<br>Asn        | GTT<br>Val        | GAA<br>Glu        | GGA<br>Gly        | CGA<br>Arg<br>295 | AGG<br>Arg        | GAT<br>Asp        | ATA<br>Ile        | CAT<br>His        | AAA<br>Lys<br>300 | GGA<br>Gly        | CAT<br>His        | CTT<br>Leu        | GAA<br>Glu        | , 912    |
| GAA<br>Glu<br>305 | AAG<br>Lys        | AAA<br>Lys        | GAT<br>Asp        | GGT<br>Gly        | TCA<br>Ser<br>310 | ATA<br>Ile        | AAA<br>Lys        | CCA<br>Pro        | GAA<br>Glu        | CAA<br>Gln<br>315 | AAA<br>Lys        | GAA<br>Glu        | GAT<br>Asp        | AAA<br>Lys        | TCT<br>Ser<br>320 | 960      |
| GCT<br>Ala        | GAC<br>Asp        | ATA<br>Ile        | CAA<br>Gln        | AAT<br>Asn<br>325 | CAT<br>His        | ACA<br>Thr        | TTA<br>Leu        | GAG<br>Glu        | ACA<br>Thr<br>330 | GTA<br>Val        | AAT<br>Asn        | ATT<br>Ile        | TCT<br>Ser        | GAT<br>Asp<br>335 | GTT<br>Val        | 1008     |
| AAT<br>Asn        | GAT<br>Asp        | TTT<br>Phe        | CAA<br>Gln        | ATA<br>Ile        | AGT<br>Ser        | AAG<br>Lys        | TAT<br>Tyr        | GAG<br>Glu        | GAT<br>Asp        | GAA<br>Glu        | ATA<br>Ile        | AGT<br>Ser        | GCT<br>Ala        | GAA<br>Glu        | TAT<br>Tyr        | 1056     |

340 345 350 GAC GAT TCA TTA ATA GAT GAA GAA GAT GAT GAA GAC TTA GAC GAA 1104 Asp Asp Ser Leu Ile Asp Glu Glu Glu Asp Asp Glu Asp Leu Asp Glu 355 TTT AAG CCT ATT GTG CAA TAT GAC AAT TTC CAA GAT GAA GAA AAC ATA Phe Lys Pro Ile Val Gln Tyr Asp Asn Phe Gln Asp Glu Glu Asn Ile 1152 370 375 GGA ATT TAT AAA GAA CTA GAA GAT TTG ATA GAG AAA AAT GAA AAT TTA 1200 Gly Ile Tyr Lys Glu Leu Glu Asp Leu Ile Glu Lys Asn Glu Asn Leu 395 GAT GAT TTA GAT GAA GGA ATA GAA AAA TCA TCA GAA GAA TTA TCT GAA 1248 Asp Asp Leu Asp Glu Gly Ile Glu Lys Ser Ser Glu Glu Leu Ser Glu 405 410 1296 🚰 u Lys Ile Lys Lys Gly Lys Lys Tyr Glu Lys Thr Lys Asp Asn Asn 420 TTT AAA CCA AAT GAT AAA AGT TTG TAT GAT GAG CAT ATT AAA AAA TAT 1344 Phe Lys Pro Asn Asp Lys Ser Leu Tyr Asp Glu His Ile Lys Lys Tyr 435 AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA TTC ATA AAA TCA 1392 Lys Asn Asp Lys Gln Val Asn Lys Glu Lys Glu Lys Phe Ile Lys Ser 450 TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT 1440 Heu Phe His Ile Phe Asp Gly Asp Asn Glu Ile Leu Gln Ile Val Asp 465 470 475 GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA 1482 Glu Leu Ser Glu Asp Ile Thr Lys Tyr Phe Met Lys Leu

#### (2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..12
  - (x) PUBLICATION INFORMATION:
    - (H) DOCUMENT NUMBER: WO 92/13884
    - (J) PUBLICATION DATE: 20-AUG-1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAG GTT ATA TAT Lys Val Ile Tyr 1

DOGODGGE D71001

12.